IN THE CLAIMS:

Amend the claims as follows:

1. (Currently Amended) A method to isolate at least one specific interaction partner ~~target molecule~~ of a compound, characterized in that said compound ~~comprising~~ comprises

a functional group that can be chemically, or enzymatically, or chemically and enzymatically altered such that an altered compound-~~target molecule~~ interaction partner complex ~~migrates~~ elutes at a different elution time with respect to the elution time of the same non-altered compound-interaction partner complex ~~differently from its unaltered version~~ in the same chromatographic separation[[,]]

a chemical structure determining the specific interaction between said compound and its interaction partner; and

a chemically reactive group which reacts with a functionality present in the interaction partner,

said method comprising the following steps:

(a) adding said compound to a complex mixture of molecules, containing 100 or more different molecules, wherein said compound stably interacts with at least one of said molecules, which is a target molecule or interaction partner, thereby forming a compound-~~target molecule~~ interaction partner complex,

(b) separating the resulting complex mixture of molecules and compound-~~target molecule~~ interaction partner complexes into multiple fractions in a first chromatographic

step wherein in a fraction derived from said chromatographic step both molecules and compound-~~target molecule~~ interaction partner complexes are [[found]]present,

(c) chemically, or enzymatically, or chemically and enzymatically altering in each fraction said compound present in at least one compound-~~target molecule~~ interaction partner complex ~~in each fraction~~, and

(d) isolating at least one ~~target molecule~~ interaction partner that interacts with said compound in a second chromatographic step, wherein the chromatography of steps (b) and (d) is performed with the same or substantially similar type of chromatography.

2. (Previously Presented) The method of claim 1, wherein said complex mixture of molecules is a complex mixture of proteins.

3. (Currently Amended) [[A]]The method according to claim 2 further comprising the cleavage of said complex ~~protein~~ mixture of proteins into a protein peptide mixture before performing step (b).

4. (Currently Amended) [[A]]The method according to claim 1 wherein said complex mixture of molecules is a protein peptide mixture.

5. (Currently Amended) A method according to claim 1~~any one of claims 1 to~~ [[4]] further comprising the step of identifying the targets.

6. (Currently Amended) The method [[of]]according to claim 5, wherein said at least one interaction partner is at least one ~~target molecules are~~ protein[[s]] or peptide[[s]] and wherein said identifying step is performed by a mass spectrometric approach ~~method selected from the group consisting of: a tandem mass spectrometric~~

~~method and/or Post-Source Decay analysis and/or measurement of the mass of the peptides~~, in combination with peptide and protein sequence database searching.

7. (Currently Amended) The method [[of]]according to claim 6, wherein the ~~measurement of the mass of the peptides in the~~ identifying step is further based on the mass of the altered compound~~combined with one or more of the following: (a) the determination of the number of free amino groups in the target peptides, (b) the cleavage specificity of the protease used to generate the protein peptide mixture; and (c) the grand average of the hydropathicity of the target peptides~~.

Claims 8-12. (Canceled)

13. (New) The method according to claim 1, wherein the compound is a drug, a drug in development, a drug lead, a drug analogue, or a drug derivative.

14. (New) The method according to claim 1, wherein the fractions of the primary chromatographic separation are pooled in such a way that elution overlap between altered compound-interaction partner complexes originating from different fractions, and between altered compound-interaction partner complexes from one fraction and molecules from one or more other fractions is avoided.